

EXHIBIT 5



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ClustalW Results

Results of search

Number of sequences
Alignment score
Sequence format
Sequence type
ClustalW version
Jalview

2
2654
Pearson
nt
1.83
[Start Jalview](#)

Output file
Alignment file
Guide tree file
Your input file

[clustalw-20070522-16041749.output](#)
[clustalw-20070522-16041749.aln](#)
[clustalw-20070522-16041749.dnd](#)
[clustalw-20070522-16041749.input](#)

[SUBMIT ANOTHER JOB](#)

To save a result file right-click the file link in the above table and choose "Save Target As".
If you cannot see the Jalview button, reload the page and check your browser settings to enable Java Applets.

Scores Table

[View Output File](#)

SeqA Name	Len (nt)	SeqB Name	Len (nt)	Score
1 U25391	715	2 SEQIDNO1	1260	23.7762
2 SEQIDNO1	1260	2 SEQIDNO1	1260	53.254

PLEASE NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

[View Output File](#)

Alignment

[Show Colors](#)[View Alignment File](#)

CLUSTAL W (1.83) multiple sequence alignment

```
U25391      TTCTTTCAATGGGAAGCAGATTGGGTACCACCCCAAGTATTGACTACCCCATCAACAAC 60
SEQIDNO1  -----

U25391      GCTATGTATTTCTGTACATTACTGCCAGCCACCATGAATATTGTACGGTACCATAAATACT 120
SEQIDNO1  -----

U25391      TGACCACCTGTAGTACATAAAACCCAATCCACATCAANNCCCCCCCCCATGCTTACAA 180
SEQIDNO1  -----

U25391      GCAAGTACAGCAACCAACCCCTCAACTATCACACATCAACTGCAGCTCCAAAGCCACTCT 240
SEQIDNO1  -----

U25391      CACCACCTAGGATACCACAACCAACCTACCCACCCTTAACAGTACATAGTACATAAAGCCAT 300
SEQIDNO1  -----

U25391      TTACCGTACATAGCACATTACAGTCAAAATCCCTTCTGTCGCCCATGGATGACCCCTCG 360
SEQIDNO1  -----GATCAGAGTCTATCACCCCTATTAACTACG 34
          *** * * * *
          * * * * *

U25391      G-AGTCTCCATGCATTTGGTATTTTCGTCTGGGGGGTGTGCACGGGATAGCATTCGGAG 419
SEQIDNO1  GGAGCTCTCCATGCATTTGGTATTTTCGTCTGGGGGGTGTGCACGGGATAGCATTCGGAG 94
          * * * * *
          * * * * *

U25391      ACGTGGAGCCGGAGCACCCCTATGTGCGAGTATCTGCTTTGATTCTGCCCATCTCTAT 479
SEQIDNO1  ACGTGGAGCCGGAGCACCCCTATGTGCGAGTATCTGCTTTGATTCTGCCCATCTCTAT 154
          * * * * *
          * * * * *

U25391      TATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTACTAAAGTGTGTTAATTA 539
SEQIDNO1  TATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTACTAAAGTGTGTTAATTA 214
          * * * * *
          * * * * *

U25391      ATTAATGCTTGTAGGACATAATAAACAATGAATGCTGCACAGCCGCTTCCACACA 599
SEQIDNO1  ATTAATGCTTGTAGGACATAATAAACAATGAATGCTGCACAGCCGCTTCCACACA 274
          * * * * *
          * * * * *

U25391      GACATATAACAAAAAATTTCCACCAAAACCCCTCCCGCCGCTTCTGGCCACAGCATT 659
SEQIDNO1  GACATATAACAAAAAATTTCCACCAAAACCCCTCCCGCCGCTTCTGGCCACAGCATT 334
          * * * * *
          * * * * *

U25391      AAACACATCTCTGCCAAACCCCAAAACAAGAACCCCTAACACCGCTAGCCAGA---- 715
SEQIDNO1  AAACACATCTCTGCCAAACCCCAAAACAAGAACCCCTAACACCGCTAACCCAGATTTC 394
          * * * * *
          * * * * *
```

```
U25391
SEQIDNO1
-----
AAATTTTATCTTTTGGCGTATGCACCTTTTAACAGTCACCCCCCAACTAACACATTATTT 454

U25391
SEQIDNO1
-----
TCCCTCCCACTCCCATACTACTATCTCATCAATACAAACCCCGCCCATCCTACCCAGC 514

U25391
SEQIDNO1
-----
ACACACACCGCTGCTAACCCCATACCCCGAACCAACCAACCCCAAGACACCCCCCA 574

U25391
SEQIDNO1
-----
CAGTTTATGTAGCTTACCTCCTCAAAGCAATACACTGAAAAATGTTAGACGGGCTCACAT 634

U25391
SEQIDNO1
-----
CACCCATAAACAAATAGGTTTGGTCCTAGCCTTCTATTAGCTCTTAGTAAGATTACAC 694

U25391
SEQIDNO1
-----
ATGCAAGCATCCCCGTTCCAGTGAGTTCACCCCTCTAAATCACCACGATCAAAAGGAACAA 754

U25391
SEQIDNO1
-----
GCATCAAGCACGCAGCAATGCAGTCAAAACGCTTAGCCTAGCCACACCCCCACGGGAAA 814

U25391
SEQIDNO1
-----
CAGCAGTGATTAAACCTTTAGCAATAAACGAAAGTTTAACTAAGCTATATACTAACCCAGGG 874

U25391
SEQIDNO1
-----
TTGGTCAATTTTCGTGCCAGCCACCCGGTTCACACGATTAAACCCCAAGTCAATAGAAGCCGG 934

U25391
SEQIDNO1
-----
CGTAAAGAGTGTTTTAGATCACCCCTCCCAATAAAGCTAAAACTAACCTGAGTTGTAA 994

U25391
SEQIDNO1
-----
AAACTCCAGTTGACACAAAAATAGACTACGAAAGTGGCTTTAACATACTGAAACACACAA 1054

U25391
SEQIDNO1
-----
TAGCTAAGACCCAAACTGCGGATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGT 1114

U25391
SEQIDNO1
-----
TAAATCAACAAAAACTGCTCGCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCT 1174

U25391
SEQIDNO1
-----
GGCGGTGCTTCATATCCCTCTAGAGAGCGCTTCTGTGAATCGATAAACCCCGATCAACC 1234
```

U25391

SEQIDNO1

TCACCACCTCTTGCTCAGCCTATATA 1260

PLEASE NOTE: Showing colors on large alignments is slow.

[Show Colors](#)[View Alignment File](#)

Guide Tree

[Show as Phylogram Tree](#)[Show Distances](#)[View DND File](#)

(U25391:0.38112, SEQIDNO1:0.38112) ;

Cladogram

U25391

SEQIDNO1

[Show as Phylogram Tree](#)[Show Distances](#)[View DND File](#)

Right-click on the above tree to see display options.
Problems printing? Read [how to print a Phylogram or Cladogram](#).

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